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1082..1085
1137..1159
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/db_xref="GI:511870"
translation="MAAKMLALPALALCALASATSHI PGHLPVMP LGTNPCMOYC
MMOGLASIMACPSLMLLOQLALPLQTPVMPDMPTNPMSPKMSKMSPLPSM,
MSOIMMPQCHDAVSQIMLOOLPFENPMAMTIPMFLOOPFGAALF"
sig_peptide
1137..1159
1200..1586
/note="10 kDa"
/product="zein protein"
polya_signal
1655..1660
BASE COUNT 782 a 506 c 471 g 803 t
ORIGIN

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Query Match 100.0%; Score 972; DB 8; Length 2562;
Best Local Similarity 100.0%; Pred. No. 1.5e-165;
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tagaataatttggtgatcgataaagatgacatgcaatcgatgtaactaat 60
Db 1591 TAGAAATATTGTTGTTATCCGCAATATGACATGACATGCGGTGACATTAAT 1650

Oy 61 taaacaataaacaagttccctctatcatcttctatctccctccatccatttgc 120
Db 1651 TAACAAATAAACAAGTTCTCTCTATTATCTTTTATATCTCTCCATATCATTTTGA 1710

Oy 121 aagccattatctcttccctccctaaagatcccaataatttgaccataattgagtc 180
Db 1711 AAGCCATTATCTCTTACCTCCCTAACTCCCAATATATTTTGGACCTTAAATGTATGTC 1770

Oy 181 atattcaaaagaatgacaataaatacagacataatacaacaacatacaataagatg 240
Db 1771 ATATTCAAAAGAATGACAAATATAGACATATATATTAATAAACATATCAATTAAGTATG 1830

Oy 241 taagaattcttaaaatgcttaaaagactaaataataatgagcaggaaggagtactatta 300
Db 1831 TATGAATCTTATAAATGCTAAAAACACACTAAATATATGAGGAGAGAGACTTTATTTA 1890

Oy 301 gtagatatactgtaattctctatctccaaataaagctcgtgtcttctcaatcaatcaat 360
Db 1891 GTAGATTACATGTATTTCTCTATCTCCAAATATAGCTGTGTTTCAATCAATCAAT 1950

Oy 361 atatatatacattgccaacatttgaatatataatcgaatgacatccgtgcagat 420
Db 1951 ATATATATGCAATGCTCAACAACTTTGAATATATATGATGACATCCGTCACAGAT 2010

Oy 421 cgtaaaaagaagcagtcaggtgcttggtcccaaaaaataatcgtcgtgtgctcagctca 480
Db 2011 CGTAAAGAAGAGCTACGCTGTGTCGCCAAAACTAATCGTCCGTTCGGHACCTTA 2070

Oy 481 taaagattctgaagagaaacaaataaaggaacataataatgaatgaatgaatgaatgaat 540
Db 2071 TAAAGATTCTGAGAGAACCAAAATTAAGGCAATATTAATTAATGATGACTCTCTCT 2130.

Oy 541 ttgaaattctgaagaaataaataaagcaaaacaaagaagaagatcaaggttaataaa 600
Db 2131 TTTCGAATTACTTAGGAATTAACATTAAGCAAAACAAAAAAGAGAGATCAAGTAAATAAA 2190

Oy 601 ggcattttgtgagaaaaacatlgagaacataagaatgcaataaataatgattgtcttc 660
Db 2191 GGCATTTTGTGAGAAAAACATGGAACATTAAGATGCAATTAATTAATGATGCTCTCTT 2250

Oy 661 atattttttatctacgtgaattctacatagataacatcgatgctcagatgataacaa 720
Db 2251 ATATTTTATTTATTCACGTAATTACATAGATGACATCGATGCTGATGATTAATCAA 2310

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Oy 721 tgaatccttagctccagagcttcgaatgaatgaatgaatgaatgaatgaatgaatgaat 780
Db 2311 TGATGCTCTAGCTCCAGAGCTTCCAAATGATGAGGATTTAAAAATCTCTATCAATTG 2370

Oy 781 ttcaaaagctcttgctcattcatgcatggcgaatgtaacctctctatataaggagtgccagc 840
Db 2371 TTCAAAAGCTCTTGTCTCATATGCTATGCGCAATGTAACCTCTATTAATAGGAGCGTCCGAC 2430

Oy 841 gtaacaattgtataaaataataattatttattcccaaatccatagcatatgctcggggagc 900
Db 2431 GTACAAATTTGTATAAATTAATATTTATTTCCCAAAATCCATGCAATATGCTCGGGAGAC 2490

Oy 901 cataatagaggatgacctcaagagctcccaattcccaatgtaacagtgtaacccatcagcataaag 960
Db 2491 CATATTTAGGGCTACCCCTCAAGGCTCTTAATTCACCTGTGAACCCCATACATTAAG 2550

Oy 961 ctgcaaaagcct 972
Db 2551 CTGCAAAAGCCT 2562

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## RESULT 2

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ZMZEILK
LOCUS ZMZEILK 570 bp mRNA linear PLN 12-SEP-1993
DEFINITION Maize mRNA for 10kDa zein.
ACCESSION X07535
VERSION X07535.1 GI:22540
KEYWORDS storage protein; zein protein.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

```

## REFERENCE

```

1 (bases 1 to 570)
AUTHORS Kirihara,J.A., Hunsperger,J.P., Mahoney,W.C. and Messing,J.W.
TITLE Differential expression of a gene for a methionine-rich storage
protein in maize
MOL. Gen. Genet. 211 (3), 477-484 (1988)
MEDLINE 88216260
COMMENT Data kindly reviewed (20 June 1988) by MESSING J.W.
FEATURES

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## FEATURES

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location/Qualifiers
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/organism="Zea mays"
/strain="W23"
/db_xref="taxon:4577"
/clone="10K2-1"
/tissue_type="endosperm"
/clone_id="pUC119"
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/note="10kDa zein (AA 1 - 150)"

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/db_xref="SPTRMBL:041881"
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MMOGLASIMACPSLMLLOQLALPLQTPVMPDMPTNPMSPKMSKMSPLPSM
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540..545
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polya_site
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/note="polyA site"

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BASE COUNT 140 a 151 c 127 g 152 t
ORIGIN

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Query Match 9.6%; Score 93.4; DB 8; Length 570;
Best Local Similarity 98.9%; Pred. No. 1.7e-07;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tagaataatttggtgatcgataaagatgacatgcaatcgatgtaactaat 60

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Db	476	TAGCAATATTTGTGGTACCGAATAAGACGTGACATGCGATGCGTACTATAT	535
Qy	61	taacaataaacaagttctcttctatctttt	95
Db	536	TAACAATAAACAAGTTCTCTTATATATATCTTTT	570
RESULT	3		
LOCUS	AX027357/c	13868 bp	DNA
DEFINITION	Sequence 5 from Patent WO0037488.		
ACCESSION	AX027357		
VERSION	AX027357.1	GI:10188332	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Thelissen, G., Delcu, W., Saedler, H. and Cacharron, J.		
TITLE	Novel mads-box genes and uses thereof		
JOURNAL	Patent: WO 0037488-A 5 29-JUN-2000;		
FEATURES			
SOURCE	1..13868		
BASE COUNT	4120 a 2725 c 2718 g 4305 t		
ORIGIN			
Query Match	9.2%; Score 89.4; DB 6; Length 13868;		
Best Local Similarity	67.4%; Pred. NO. 4.8e-07;		
Matches 126; Conservative	0; Mismatches 61; Indels 0; Gaps 0;		
Qy	128	ttatccttctatccctcaagtcgccatataatttagacctaaattgattgctcatattca	187
Db	12732	TAAATACCCCAATCAATAATAGTATTCGGCTTCTCAATTTTATATCATATCA	12673
Qy	188	aagaagatgcacataaattctagacatataataaacaacatcataagattgtatgaat	247
Db	12672	AATAGATGATGATTAATTAATTAACACATATATATTAACATATTAATCAAGTATGATGAT	12613
Qy	248	ctattcaaatatgcataaagactaatattatggagcggagagatcttctatgatgatt	307
Db	12612	CTATTAATCTTTTAAAAACCAATTTTAAATTTGGGACAAAGAGATATGAGAAATTCAAG	12553
Qy	308	acattgt 314	
Db	12552	AACATGT 12546	
RESULT	4		
LOCUS	2M27K2NB/c	3695 bp	DNA
DEFINITION	2.mays 27kda zein locus DNA.		
ACCESSION	X56118		
VERSION	X56118.1	GI:22100	
KEYWORDS	zein protein.		
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC		
JOURNAL	clade; Panicoidae; Andropogoneae; Zea.		
GENOMICS	1 (bases 1 to 3695)		
REFERENCE	Das, O.P., Ward, K., Ray, S. and Messing, J.		
SEQUENCE	Sequence variation between alleles reveals two types of copy		
CORRECTION	correction at the 27-kda zein locus of maize		
GENOMICS	11 (44), 849-856 (1991)		
REFERENCE	2 (bases 1 to 3695)		
MESSING, J.			

FEATURES	Source	Location/Qualifiers
misc_signal	1..3695	/organism="Zea mays" /strain="A18" /db_xref="taxon:4577" /tissue_type="leaf" 2195..2205
misc_signal	2448..2451	/standard_name="Proline box"
misc_feature	2482..2484	/standard_name="Cap Site"
BASE COUNT	115 a 877 c 734 g 969 t	
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Best Local Similarity	79.8%;	Prod. No. 1.4e-06;
Matches 103;	Conservative 0;	Mismatches 26; Indels 0; Gaps 0;
QY 171	ttgtagctcatatccaagaatgacacataaactagacacatataataaacacataca 230	
Db 3501	TTTTTGTCTATATTCATTAATGATGCATATTAACAATCTGATATATATATGAAAAACACATATA 3442	
QY 231	tttaagctatgttaagaatcatttaaaatgtctaaccgactaatattatggagcggagggag 290	
Db 3441	TAAATTTATGTATTAACCCATTTAAAGGTTAAATGAAATTTTAAATTTGGACAGATGAG 3382	
QY 291	tacttaatt 299	
Db 3381	TATTTT 3373	
RESULT 5		
LOCUS	AF215823	17380 bp DNA linear PLN 02-JAN-2001
DEFINITION	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) gene,	
ACCESSION	AF215823	
VERSION	AF215823.1	GI:12004293
KEYWORDS		
SOURCE	Zea mays.	
ORGANISM	Zea mays	
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS	1 (Bases 1 to 17380)	
TITLE	Cui,X.; Hsia,A.P.; Wise,R.P. and Schnable,P.S.	
JOURNAL	Alternative Transcription Start Sites and Polyadenylation Sites are	
AUTHORS	Unpublished	
TITLE	2 (Bases 1 to 17380)	
JOURNAL	Hsia,A.P., Chen,W. and Schnable,P.S.	
AUTHORS	Submitted (13-DEC-1999)	
TITLE	Agromony Hall, Ames, IA 50011, USA	
JOURNAL	Location/Qualifiers	
FEATURES	1..17380	
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misc_feature	join(3120..3472,5369..5515,6042..6184,6272..6425,6533..6762,13928..14017,14115..14288,14381..14518,14863..15000,15119..15180,15304..15869)	

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PLMAYAKVGPALACGNTLVKTAECTPLSALYSKLLHAGLPEGVNVVSGFPTA
GAALASHMDVDKIATFSTDTGKILLEAKSNLKTVLELGGKSPFIIMDDADVDA
VELAHALPEFNGGCCGSRTPFHERVDEFEKARAKRKYVNDGPRKRGVGGP
IDDDPQNKILIRYGVNDGACATLVTCGDRGCGFIQPIIISDVODGKIKQEEIRG
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4875..5240
/gene="rf2"
/note="similar to regions in Zea mays Ama, CHI, Incw3,
PHYTII and hml genes"
6763..13927
/gene="rf2"
/note="putative copia-like retroposon element"
BASE COUNT 4048 a 4729 c 3855 g 4748 t
ORIGIN
Query Match 9.0% Score 87; DB 8; Length 17380;
Best Local Similarity 74.5% Pred. No. 1.2e-06;
Matches 123; Conservative 0; Mismatches 40; Indels 2; Gaps 1;
Qy 136 taccctcaagtcctcaatattttagaacctaaattgtatgctcatcaatcaagaatg 195
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Db 13593 TACTCCCTCGCTCCACAAAGCTTTATCATCTGCTTTTATATATATATCAATTAATA 13652
Qy 196 acaatbaatcagacatataataaacacatcaatgaatgatacgaatcatataa 255
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Db 13653 ATATGATATCTAGAC--ACATACAAACACATACACTAATATTGTATGTAATCATTAA 13710
Qy 256 atcctaaagactaatattatggagcggaggagctactatata 300
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Db 13711 AGGCTAAATGATTTTATTGGAACATAGGAGTATTATTCTAA 13755
RESULT 6
AF466203 147198 bp DNA linear PLN 07-FEB-2002
AF466203/c LOCUS
DEFINITION Zea mays clone ZMBRC-0092E12 putative RIR2 orf3, putative
gypsy-type retrotransposon RIR2, putative orf1, regulatory
protein, putative pol protein, putative pol protein, putative gag
protein, putative pol protein, putative cis-zeatin
O-glucosyltransferase, putative gag-pol precursor -orf1, putative
prpol, putative gag-pol precursor -orf2, and putative prpol genes,
complete cds.
ACCESSION AF466203
VERSION AF466203
KEYWORDS
SOURCE
ORGANISM Zea mays.
Ze mays.
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 147198)
AUTHORS Ramakrishna, W., Sanmiquel, P., Emberton, J. and Bennetzen, J.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Department of Biological Sciences, Purdue
University, West Lafayette, IN 47907, USA
REFERENCE 2 (bases 1 to 147198)
AUTHORS Llaça, V., Linton, E. W., Young, S., Koychook, S. and Messing, J.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Rutgers, The State University of New
Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute,
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Location/Qualifiers
1..147198
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/db_xref="taxon:4577"
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7419..7764,7846..8336)
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5148..8336
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GI:17082476"
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RRRARLEKRCROOREGGLREPSPETDDDDDDDDDEEDMDMARLGISGCGCGE
PSSQPSGPPPSVYGVGASGSMWEANGRRRPPDSAGCAEYARPGVBARAPGPL
VPAHGDPOYLATVPPEPSAPRASKRVAKLPVRRSSAAVSGAGIDSTSOAMIA
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6215..6234
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/gene="2092E12.2"
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TITLE Direct Submission  
JOURNAL Submitted (12-APR-2001) Wakeman Institute, Rutgers University, 190  
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA  
REMARK Sequence update by submitter  
REFERENCE 5 (bases 1 to 346296)  
AUTHORS Song, R., Liaca, V. and Messing, J.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-2001) Wakeman Institute, Rutgers University, 190  
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA  
REMARK Amino acid sequence updated by submitter  
COMMENT On Apr 12, 2001 this sequence version replaced gi:4416300  
gi:4140633.

FEATURES  
Source Location/Qualifiers  
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/clone="cosmid II.2E10"  
/note="inbred line BSS53"  
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/db\_xref="taxon:4577"  
/chromosome="4"  
/map="4s"  
/clone="cosmid III.3C12; V.9D7"  
/note="inbred line BSS53"  
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1261..185036  
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/db\_xref="taxon:4577"  
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DHPPCTAGIGSEVLEPKRKTVLDPSPLEPHYIOESAATNMLBALDNDRGLTSKQILRST  
GMPDPKRVKVLNNOEALISLMKIDPOAAK"  
15142..17012  
/note="similar to cell division protein FTS2"  
22068..22142  
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24303..24307  
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24306..31758  
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24308..24976  
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25532..26569  
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Best Local Similarity 93.3%; Pred. No. 0.00081;  
Matches 84; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
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Db 301418 ACCCCATCAGCTAAGCTCAAGAGCCT 301447  
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LOCUS  
DEFINITION  
Zea mays clone ZMMBb-2195D10 putative transposase gene, partial  
cds: glycy1-tRNA synthetase, ornithine carbamoyltransferase,  
putative gag protein, putative SET-domain transcriptional  
regulator, putative oxysterol-binding protein, putative  
polyprotein, putative oxysterol-binding protein, putative  
polyprotein, putative phosphatidylinositol-4-phosphate-5-kinase,  
hypothetical protein, putative gag-poli polyprotein, putative  
polyprotein, putative retrotransposon protein, and pipol genes,  
complete cds; and putative teosinte branched2; TB2 gene, partial  
cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 141939)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (07-JAN-2002) Department of Biological Sciences, Purdue  
University, West Lafayette, IN 47907, USA  
2 (bases 1 to 141939)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (07-JAN-2002) Genetics Department, University of  
Wisconsin, Madison, WI 53706, USA  
3 (bases 1 to 141939)  
REFERENCE

AUTHORS  
TITLE  
JOURNAL  
Llaça, V., Linton, E.W., Young, S., Kovchok, S. and Messing, J.  
Direct Submission  
Submitted (08-JAN-2002) Rutgers, The State University of New  
Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute,  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
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1. 141939  
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Query Match          7.2%: Score 69.8; DB 8; Length 141939;
Best Local Similarity 96.5%: Pred. No. 0.001;
Matches 82: Conservative 0; Mismatches 2; Indels 1; Gaps 1

OY  889  tctgtcgggaccataattagggggtaccctcaaggctccattctcagctgtga-ccc 947
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DB  8479  TTTTCTGGGGGACCATATTATTTAGGGTACCCCAAGGCTCTCTAATTCAGCTGTAAACCC 8420
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY  948  catcagcataaagctgcaaaagcct 972
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  8419  CATCAGCACAAAGCTGCMAAGGCTT 8395

RESULT  11
AP004668 140465 bp DNA linear HTG 24-JAN-2002
LOCUS
DEFINITION
Oryza sativa chromosome 7 clone P0475E07, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
AP004668
AP004668.1 GI:18307746
HTG; HTGS_PHASE2.
Oryza sativa (cultivar:Nilponbare) DNA, clone:P0475E07.
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriurtoideae; Oryzaceae; Oryza.
1 (bases 1 to 140465)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (23-JAN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondei
2-1-7, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: it currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
location/Qualifiers
1..140465
/organism="Oryza sativa"
/cultivar="Nilponbare"
FEATURES
source

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...

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 00:45:13 ; Search time 201.54 Seconds  
(without alignments)  
8280.445 Million cell updates/sec

Title:	US-09-763-329-1
Perfect score:	972

Sequence: 1 tagaataattgtgtgtat.....gcataagctgcaagcct 972

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : N\_Genseq/02802.\*

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2:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA1981.DAT.*
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4:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA1983.DAT.*
5:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA1984.DAT.*
6:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA1985.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	972	100.0	972	21	AA293518	dzrl gene 3' UTR r
2	972	100.0	2562	19	AAV70953	Zea mays 10 kDa ze
3	89.4	9.2	13868	21	AAAS1324	Z. mays MADS-box p
4	82.4	8.5	1203	21	AAAC48017	Zea mays DNA fragm
5	69.4	7.1	2710	13	AAO20749	Sequence of the pr
6	68.8	7.1	879	22	AAAF81456	Corn promoter clon
7	68.8	7.1	879	22	AAAF81457	Corn promoter clon
8	67.2	7.0	2661	15	AAO51873	Sequence comprisin
9	59.2	6.1	4936	24	AA519028	Maize Ramona 1 cod

C	10	56	5.8	17594	24	AAFL34027	Human immune system
C	11	54.2	5.6	631	22	AAE81465	Corn promoter clone
C	12	54.2	5.6	2722	21	AAC86507	DNA compising a b
C	13	54.2	5.6	2722	21	AAC86508	DNA construct comp
C	14	54.2	5.6	3991	22	MAD16633	Human novel protei
C	15	54.2	5.6	5173	20	AAZ081721	Chimeric gene cons
C	16	54.2	5.6	5392	20	AAZ08720	Chimeric gene cons
C	17	54.2	5.6	5622	21	AAC86506	DNA construct comp
C	18	52.8	5.4	8576	24	ABL34228	Human immune syste
C	19	52.6	5.4	5360	20	AAZ08717	Chimeric gene cons
C	20	51.6	5.3	2418	13	AAZ08286	P. falciparum GPI3.1
C	21	51.2	5.3	8375	24	ABL33079	Human immune syste
C	22	51	5.2	547	24	ABL32713	Human immune syste
C	23	50.4	5.2	2437	24	ABL34350	Human immune syste
C	24	50.4	5.2	15689	22	AA545396	Chemically pretrea
C	25	50	5.1	6032	24	ABL34221	Human immune syste
C	26	49.8	5.1	5379	24	ABL33677	Human immune syste
C	27	49.8	5.1	5379	24	ABL33677	Human immune syste
C	28	49.8	5.1	18154	24	ABL34577	Human metastasis a
C	29	49.2	5.1	1428	21	AAZ09466	Sakuranetin synthas
C	30	49.2	5.1	4371	21	AAA99467	Sakuranetin synthas
C	31	49.2	5.1	5241	21	AAZ09467	Sakuranetin synthas
C	32	49	5.0	8210	24	AA561283	Human gene regulat
C	33	48.4	5.0	6503	24	ABL32770	Human immune syste
C	34	48.4	5.0	19659	24	ABL32766	Human immune syste
C	35	48.2	5.0	15548	24	ABL34155	Human immune syste
C	36	47.8	4.9	5518	18	AAV73870	Cotton fibre promom
C	37	47.8	4.9	5547	18	AAV73865	Cotton fibre promom
C	38	47.8	4.9	17869	24	ABL32105	Human immune syste
C	39	47.4	4.9	9483	24	ABL33376	Human immune syste
C	40	47.4	4.9	9483	24	AA561091	Human gene regulat
C	41	47.2	4.9	5945	24	ABL33085	Human immune syste
C	42	47.2	4.9	17280	22	AA546771	Tumour suppressor
C	43	47.2	4.9	17389	24	ABL33414	Human immune syste
C	44	47.2	4.9	61020	22	AA546788	Tumour suppressor
C	45	47	4.8	6065	24	ABL32505	Human immune syste

	RESULT	1
ID	AAZ93518	
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AC	AAZ93518;	
XX		
D1	24-JUL-2000 (first entry)	
XX		
DE	dzrl gene 3' UTR region.	
XX		
KW	Maize; corn; methionine; zein storage protein; delta zein; dzrl;	
XX	transgenic plants; gene expression; promoter; UTR;	
XX	untranslated region; ss.	
OS	Zea mays.	
PN	WO200012681-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	25-AUG-1999; 99WO-US20308.	
XX		
PR	27-AUG-1998; 98US-0098034.	
XX		
PR	07-JUN-1999; 99US-0137836.	
XX		
PA	(RUTF ) UNIV RUTGERS STATE NEW JERSEY.	
XX		
PI	Messing J, Lai J;	
DR	WPI; 2000-237865/20.	
XX		
XX		

DNA construct used for producing transgenic maize plants that express

PT high quantities of 10 kilodalton zein seed storage protein encodes  
PT delta-zein operably linked to promoter and to sequence encoding  
PT modified 3' untranslated region  
XX  
XX  
PS Disclosure; Page 48; 54pp; English.  
CC New DNA constructs are described which encode a delta-zein operably  
CC linked to a promoter and to a modified 3' untranslated region (UTR),  
CC devoid of binding sites for a dzrl negative regulatory protein.  
CC The DNA construct is useful for producing transgenic maize plants  
CC that express high quantities of the 10 kilodalton methionine rich  
CC zein seed storage protein. Overexpression of the zein storage protein  
CC in maize seeds increases the capture of free methionine during plant  
CC maturation, which otherwise would be lost. The transgenic plants are  
CC superior to prior art natural high-methionine variants because they  
CC consistently express the 10 kilodalton transgene regardless of the  
CC dzrl allelic composition of the variety. This sequence is the wild  
CC type 3'UTR region of maize prior to modification.  
XX  
XX  
SQ Sequence 972 BP; 329 A; 168 C; 157 G; 318 T; 0 other;

Query Match 100.0%; Score 972; DB 21; Length 972;  
Best Local Similarity 100.0%; Pred. No. 3,3e-192;  
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 tagaataatctgtctgtatcgaataatgagtcgacgcatcgctgtgactcatat 60  
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DB 61 taacataataaagaagtcctctatattctttatattctctccatccattttgca 120  
QY 121 aagccatactccttactcctcctcctcctcctcctcctcctcctcctcctcctc 180  
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DB 121 aagccatactccttactcctcctcctcctcctcctcctcctcctcctcctcctc 180  
QY 181 atattcaaaagaatgcgaataataatctagaacataatataaaacataatagaatttg 240  
DB 181 atattcaaaagaatgcgaataataatctagaacataatataaaacataatagaatttg 240  
QY 241 taagaaatctaaatgtcctaaagcactaatatataatgagcaggaggaactactta 300  
DB 241 taagaaatctaaatgtcctaaagcactaatatataatgagcaggaggaactactta 300  
QY 301 gtgaatctacatgtttcttctctatctcctatccaaataaagctcgttttcaatcaatca 360  
DB 301 gtgaatctacatgtttcttctctatctcctatccaaataaagctcgttttcaatcaatca 360  
QY 361 atatatccatgcgtccaaacatttgaattatatactcagggtgacatccgttcacagat 420  
DB 361 atatatccatgcgtccaaacatttgaattatatactcagggtgacatccgttcacagat 420  
QY 421 cgtaaagaagcagtcacggtgtgtgtcccaaaaataatcgtctcgttgcgttaccctta 480  
DB 421 cgtaaagaagcagtcacggtgtgtgtcccaaaaataatcgtctcgttgcgttaccctta 480  
QY 481 taagaaatctaaagcagcacaataaagcacaataaataatcgttcaatataatgactcctct 540  
DB 481 taagaaatctaaagcagcacaataaagcacaataaataatcgttcaatataatgactcctct 540  
QY 541 ttgaatctacttgagatacacaataaagaagaagaagaagaagaagaagaagaagaagaaga 600  
DB 541 ttgaatctacttgagatacacaataaagaagaagaagaagaagaagaagaagaagaagaaga 600  
QY 601 ggcattctgtgagaacaatgcgaacataagaatgacataagtaagtgtgtctctt 660  
DB 601 ggcattctgtgagaacaatgcgaacataagaatgacataagtaagtgtgtctctt 660  
QY 661 atattcttcttctcagtgaaattacataagatcacatcgagatttcgattgaaatacaa 720  
DB 661 atattcttcttctcagtgaaattacataagatcacatcgagatttcgattgaaatacaa 720

QY 721 tgaatccttagctcgcgagagcttcgaatgataagcagatttaaaatactcctaactg 780  
DB 721 tgaatccttagctcgcgagagcttcgaatgataagcagatttaaaatactcctaactg 780  
QY 781 ttggaagtcttctgtctatcatcagggcaatgacctcattatagaggagcgtgcac 840  
DB 781 ttggaagtcttctgtctatcatcagggcaatgacctcattatagaggagcgtgcac 840  
QY 841 gtacaatttgttaaaattatattttatcccaaatccataigcatatgttcggggac 900  
DB 841 gtacaatttgttaaaattatattttatcccaaatccataigcatatgttcggggac 900  
QY 901 cataataggggagccttaagcctcctaatttcacgttgtaaccccttcgacataag 960  
DB 901 cataataggggagccttaagcctcctaatttcacgttgtaaccccttcgacataag 960  
QY 961 ctgcaaaagcct 972  
DB 961 ctgcaaaagcct 972

RESULT 2  
AAV70953  
ID AAV70953 standard; DNA; 2562 BP.  
XX  
XX AAV70953;  
AC  
XX  
XX 23-AUG-1999 (first entry)  
XX  
DE Zea mays 10 kDa zein gene DNA sequence.  
XX  
XX  
XX Non-glycogen-like polysaccharide production; fermentation; zein gene;  
KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;  
KW non-starch branching gene; amylopectin; amylose; plant-like starch; ss.  
XX  
OS Zea mays.  
XX  
PN M09844780-A1.  
XX  
PD 15-OCT-1998.  
XX  
XX 03-APR-1998; 98MO-US06660.  
PF  
XX  
PR 04-APR-1997; 97US-0042939.  
XX  
PA (EXSE-) EXSEED GENETICS LLC.  
XX  
PI Guan H, Keeling PL;  
XX  
DR WPI; 1998-568285/48.  
XX  
DR P-PSDB; AAV70887.  
XX  
PT Producing non-glycogen-like polysaccharides in bacteria, fungi or  
PT plants - transformed with genes for enzymes involved in starch or  
PT glycogen synthesis allows fermentative production of starches with  
PT engineered properties  
XX  
XX  
XX Disclosure; Fig 45a; 150pp; English.  
PS  
XX The specification describes a method for the production of  
CC non-glycogen-like polysaccharides in a host. The method comprises  
CC transforming a host, suitable for fermentation, with genes encoding  
CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.  
CC The specification also describes hosts transformed with a gene active  
CC in glycogen synthesis and at least one non-starch branching gene,  
CC involved in production of amylopectin or amylose in its original host.  
CC The method is used to produce plant-like starches by fermentation and  
CC new starches in plants. These starches are useful for all food and  
CC non-food applications of starch. The present sequence is used in  
CC the course of the invention.  
SQ Sequence 2562 BP; 782 A; 506 C; 471 G; 803 T; 0 other;

Query Match	100.0%;	Score 972;	DB 19;	Length 2562;
Best Local Similarity	100.0%;	Pred. No. 3.8e-192;		
Matches 972; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	taaaatatttggtgtgatacgaataaagatgtgaacgaatcggtgtgactcaatt	60
Db	1591	taagaatatttggtgtgatacgaataaagatgtgaacgaatcggtgtgactcaatt	1650
OY	61	taacaataaacaagtttcctcttaattctttatatactctccataccatttgcga	120
Db	1651	taaccaataaacaagtttcctctcttcttattctttatatactctccataccatttgcga	1710
OY	121	aagccattactcttactcccttaagtcctcaatattttgacctaaattttatgttc	180
Db	1711	aagccattactcttactcccttaagtcctcaatattttgacctaaattttatgttc	1770
OY	181	atatcnaaagaatgacaataaactaagacalatatataaacaacacacattgaagtatg	240
Db	1771	atttcnaaagaatgacaataaactaagacalatatataaacaacacacattgaagtatg	1830
OY	241	taagaattctatnaaaatgttaaaagactaattatttgggacggaggaattacttatta	300
Db	1831	taagaactctatnaaaatgttaaaagactaattatttgggacggaggaattacttatta	1890
OY	301	gtgacttaacatgtttatttcttcctctatcccaataaagtcggttttccataccaatcaat	360
Db	1891	gtgacttaacatgtttatttcttcctctatcccaataaagtcggttttccataccaatcaat	1950
OY	361	atatattacaatgttccaaacattttgaattatatacttaagtgtgagaatcccgacagat	420
Db	1951	atatattacaatgttccaaacattttgaattatatacttaagtgtgagaatcccgacagat	2010
OY	421	cgtaaaagaagcagtcacggtgtgtgtcccaaaaactaatcgctcgttttcggttcaacctta	480
Db	2011	cgtaaaagaagcagtcacggtgtgtgtcccaaaaactaatcgctcgttttcggttcaacctta	2070
OY	481	taaaagtttaagaaggaacccaataaaggacatataattatgttaataagactctctcc	540
Db	2071	taaaagttcttgaaggaacccaataaaggacatataattatgttaataagactctctcc	2130
OY	541	tcttgaattactcttgaataatacaataagcaacaanaaaaggagaagatccaaggttaaataa	600
Db	2131	tcttgaattactcttgaataatacaataagcaacaanaaaaggagaagatccaaggttaaataa	2190
OY	601	ggcatttttggagaanaaccttgaagacataagatgcataaatlaattgtttgtctctctt	660
Db	2191	ggcatttttggagaanaaccttgaagacataagatgcataaatlaattgtttgtctctctt	2250
OY	661	atcttttttttacttcaacggaattatacaataatccatcagatcttcgactggttaatacaa	720
Db	2251	atatttttttttacttcaacggaattatacaataatccatcagatcttcgactggttaatacaa	2310
OY	721	tgtatgccttaagctccgagagacttgaatgataagagatlttaaaaaatbctccatcaatg	780
Db	2311	tgtatgccttaagctccgagagacttgaatgataagagatlttaaaaaatbctccatcaatg	2370
OY	781	tctgaagaagtctctgtctcatgcatgacgggcaatgtaaccccttataataggaacggttcgac	840
Db	2371	tctgaagaagtctctgtctcatgcatgacgggcaatgtaaccccttataataggaacggttcgac	2430
OY	841	gtacaaaatttgtataaaatlatattttatltcccaaatccctatgacatagttgtccggagac	900
Db	2431	gtacaaaatttgtataaaatlatattttatltcccaaatccctatgacatagttgtccggagac	2490
OY	901	caataatgaaggtacccctcaagagccctcaattcccaagctgtgttaaccccaacagatataag	960
Db	2491	caataatgaaggtacccctcaagagccctcaattcccaagctgtgttaaccccaacagatataag	2550
OY	961	ctgcgaagaagcct 972	
Db	2551	ctgcgaagaagcct 2562	

RESULT	3
AAA51324/C	
ID	AAA51324 standard; DNA; 13868 BP.

AC AAA51324

DT 26-SEP-2000 (first entry)

DE 2. may MADS-box protein ZMM14 gene regulatory sequence.

KN ZMM14; maize; MADS-box; DNA-binding; upper floret; spikelet;  
KN inflorescence; grass; chromosome 1; monocotyledon; regulatory region;  
KN disease resistance; flowering; growth regulator; herbicide; OSMADSL; ds

OS Zea mays

PN WO200037488-A2.

PD 29-JUN-2000

PF 20-DEC-1999; 99WO-EP10116.

PR 21-DEC-1998; 98EP-0124335.

PR 29-OCT-1999; 99EP-0121591.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Cacharron J, Theissen G, Deleu W, Saedler H;

DR WPI; 2000-452177/39.

PT Novel nucleic acids encoding proteins with the activity of proteins  
PT expressed in the upper florets of spikelets of grass inflorescences  
PT useful for producing plants with altered proteins levels or  
PT compositions

PS Disclosure; Page 88-91; 93pp; English

CC This is a regulatory region sequence from the maize (Zea mays) ZmM14  
CC gene which encodes a MYC-type MADS-box protein. The protein is involved  
CC in DNA-binding and is expressed in the upper florets of spikelets of  
CC grass inflorescences. The ZmM0 and ZmM14 genes (see AAtS1322-23) map to  
CC chromosomes 1 and 9, respectively, and are similar to OSMA51 from rice  
CC (Oryza sativa). The ZmM8 and ZmM14 genes are useful for study of  
CC MADS-box proteins in monocotyledons. The sequences can be used to  
CC produce transgenic plants having altered level or composition of  
CC protein(s) in the florets of spikelets, for modulating the number of  
CC kernels, for conferring or improving disease resistance, generating late  
CC or early flowering, expressing heterologous proteins in the upper floret  
CC in the spikelets of grass inflorescence, modifying solute partition in  
CC florets, improving kernel derived products or the expression of enzymes  
CC affecting any agronomic aspect of the kernel or the whole inflorescence.  
CC Compounds identified as being activators or inhibitors of genes  
CC specifically expressed in the spikelets of grass inflorescence may be  
CC used as growth regulators and/or herbicides.

SQ Sequence 13868 BP; 4120 A; 2725 C; 2718 G; 4305 T; 0 other;

Query Match	9.28;	Score 89.4;	DB 21;	Length 13868;
Best Local Similarity	67.48;	Pred. No. 2.1e-09;		
Matches 126;	Conservative	0;	Mismatches 61;	Indels 0;
			Gaps	0;

QY 128 ttatccttactccctaagtcccaatatattttagacctaaattgtatgtctatatcca 187

Db 12732 TAATACTCCCATTTCTAAATAGTATTCGCTTTAGCTCTCAATTTTATGTCTATATCCA 12673

QY 188 aaagaatgacaataatctagacatatataaaacacatacatltaagtattgtatgaat 247

Db 12672 AATGATGATGAATCTAAACACATATATAAACATATTAATCAAGTATGGTATGAAT 12613

OY 248 ctattaaatgctaaacgactaataatcattcggacggaggagtaacttattagtagatt 307  
Db 12612 CTATTGATTTTAAAAACGAAATTTTAATTTGGGACAAAGACGACTATATGGAATTTCAAG 12553  
OY 308 acattgc 314  
Db 12552 AACATCT 12546  
RESULT 4  
AAC48017/c  
ID AAC48017 standard; DNA: 1203 BP.  
XX  
AC AAC48017:  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Zea mays DNA fragment SEQ ID NO: 55961.  
XX  
KM Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic;  
KM pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 22-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 15-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134210.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 18-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138647.

PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144082.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145091.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145224.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0146389.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.





Only Match	7.1%	Score 69.4	DB 13.4	Length 2710
Best Local Similarity	92.3%	Pred. No. 2,3e-05		
Matches	84	Conservative	0	Mismatches 6
				Indels 1
				Gaps 1
OY	883	ttcatatctgctggagacccaataattaggagctctaaagctcctcaattctcagctcgt	942	
Db	2340	tcgaanaagctctcggggcccaataattcgggttaaccttaagctcctcaattctcagctcgt	2399	
OY	943	aaccc-calcagcataaagctctgcaagctc	972	
Db	2400	aacctccatctcagctgtaagctgcaagctc	2430	

RESULT 6  
 ID AAF81456 standard; DNA; 879 BP.  
 AC AAF81456;  
 DT 08-JUN-2001 (first entry)  
 DE Corn promoter clone #700164347 #1.  
 KW Corn; promoter; transgenic plant; herbicide resistance; ds.  
 XX Zea mays.  
 OS  
 PN MO200119976-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PE 13-SEP-2000; 2000MO-US25078.  
 XX  
 PR 16-SEP-1999; 99US-0154182.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Anderson HM, Chay CA, Chen G, Conner TW;  
 XX  
 DR WPI: 2001-244796/25.  
 XX  
 PT Novel promoter nucleic acid sequences useful for regulating  
 PT heterologous gene expression in plants, comprising regulatory sequences  
 PT located upstream to plant DNA structural coding sequences  
 XX  
 PS Claim 1: Page 90; 101pp; English.  
 XX  
 XX The present invention relates to novel corn promoter sequences (see  
 CC AAF81456-AAF81478). The promoter sequences are useful for conferring  
 CC expression of a second polynucleotide molecule in a transgenic plant  
 CC tissue. In addition, the promoter sequences are useful for providing  
 CC plants with herbicide resistance. The promoter sequences are suitable for  
 CC selectively modulating expression of an operatively linked gene and  
 CC provide additional regulatory element diversity in a plant expression  
 CC vector in gene stacking approaches. The present sequence is one such corn  
 CC promoter sequence isolated in the present invention.  
 XX  
 XX Sequence 879 BP; 264 A; 192 C; 136 G; 287 T; 0 other;

Query Match	Similarity	7.11	Score	68.8	DB	22	Length	879
Best Local	Similarity	63.84	Pred.	No.	2.6e-05			
Matches	123	Conservative	0	Mismatches	72	Indels	1	Gaps
QY	152	atataatttagccttaattatgtatgttcattatataaagaatcacatataatctagca	211					
DB	231	atcgcgttttagcctcttgatctttaaagtcctcacatcata -cattatgataatatagaca	289					
QY	212	tatatataaacacatatacattgaattatgtatgaatacattataaagtcataaagcactaa	271					
DB	290	tatgcatgagaacatatcacacaaatctgtatgaatgtagtcacaaatccaaactcattt	349					

[illegible]

RESULT 7  
 ID AAF81457  
 XX AAF81457 standard; DNA: 879 BP.  
 AC AAF81457;  
 XX  
 DT 08-JUN-2001 (first entry)  
 XX  
 DE Corn promoter clone #700164347 #2.  
 XX  
 KW Corn; promoter; transgenic plant; herbicide resistance; ds.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200119976-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 13-SEP-2000; 2000WO-US25078.  
 XX  
 PR 16-SEP-1999; 99US-0154182.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Anderson HM, Chay CA, Chen G, Conner TW;  
 DR WPI: 2001-244796/25.  
 XX  
 XX Novel promoter nucleic acid sequences useful for regulating  
 PT heterologous gene expression in plants, comprising regulatory sequences  
 PR located upstream to plant DNA structural coding sequences -  
 XX  
 PS Claim 1; Pages 90-91; 101pp; English.  
 XX  
 CC The present invention relates to novel corn promoter sequences (see  
 CC AAF81456-AAF81478). The promoter sequences are useful for conferring  
 CC expression of a second polynucleotide molecule in a transgenic plant  
 CC tissue. In addition, the promoter sequences are useful for providing  
 CC plants with herbicide resistance. The promoter sequences are suitable  
 CC for selectively modulating expression of any operatively linked gene and  
 CC provide additional regulatory element diversity in a plant expression  
 CC vector in gene stacking approaches. The present sequence is one such corn  
 CC promoter sequence isolated in the present invention.  
 XX  
 XX Sequence 879 BP; 264 A; 192 C; 136 G; 287 T; 0 other:

	Query Match	Similarity	7.1%	Score 68.8	DB 22	Length 879
Best Local	Similarity	62.8%	Pred. No. 2.6e-05			
Matches 133	Conservative	0	Mismatches	72	Indels	1
						Gaps 1
Qy	152	atatacttagagccttaattgtagtgcataatcacaagaatgacaataactatgaca	211			
Db	231	atctcgctttagctctgattgttaagtgtctcaatcacta-catgtagtacaataatagca	289			
Qy	212	tatatataaacacatacatatgaatgtatgtatgaatcattatataaattgctaaagaacaa	271			
Db	290	tatgcatagaacaatatcaccaaatctttagatgtgccttaaatatccaaataaattt	349			
Qy	272	tatttatggagagggagggagactttttgtgatataatgttatcttctctatccaa	331			
Db	350	tatttgatgcttcagagggagagatcttaataacaagatctgtcctaaagtttggctccaccaa	409			



ID ABL34027 standard; DNA: 17594 BP.  
XX  
XX ABL34027:  
AC  
XX  
XX  
XX 26-MAR-2002 (first entry)  
DE Human immune system associated gene SEQ ID NO: 2000.  
XX  
XX Human: immune system disease; cytosine methylation; antiscratic;  
KW antiarteriosclerotic; antianemic; cytosolic; noctropic;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antihemagic; antihypertic; antidiabetic; antipsoriatic;  
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W0200200928-AZ.  
XX  
XX  
XX PD 03-JAN-2002.  
XX  
XX PF 02-JUL-2001; 2001WO-EP07537.  
XX  
XX PR 30-JUN-2000; 2000DE-1032529.  
XX PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX PA (EPIC-) EPIGENOMICS AG.  
XX  
XX PI Olek A, Plepenbrock C, Berlin K;  
XX  
XX WPI: 2002-130909/17.  
DR  
XX  
XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation.  
XX  
XX  
XX PS Claim 1; SEQ ID NO 2000; 32pp + Sequence Listing; German.  
XX  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
CC  
XX  
XX Sequence 17594 BP; 5843 A; 96 C; 3426 G; 8229 T; 0 other:  
SQ  
Query Match 5.8%; Score 56; DB 24; Length 17594;  
Best Local Similarity 46.1%; Pred. No. 0.018;  
Matches 261; Conservative 0; Mismatches 300; Indels 5; Gaps 2;  
OY 127 attatcccttaccctccctgaagtcacatatacttttagaccttaactgaagctatctc 186  
DB 14736 ATATATCCAAACACACATCTCTTAATCTTTTAAAAATATACATATATATATATAC 14677  
OY 187 aaaaagaaagacataaactagacataataaacaacataacataagatgtgag 246  
DB 14676 ATATTAATTAACATATTTATATATATATATATACATATTTATATATATATATAT 14617  
OY 247 tccatcaaaatctaaagacataataatgagagcgagagagacttaactgaagtagat 306  
DB 14616 AT 14557  
OY 307 ---taacattgtaattcttcctacatccaaataaagctgagtttccaatcaatcaata 363  
DB 14556 AT 14497  
OY 364 tatatacaatgccaacacatttgaaatataatacchaggctgagatccggacagatcgt 423

DB 14496 AACTTACCTCTTAAAAAAGAAAAAATATTTATTAATTAATTAATTAATTAATTAAT 14437  
OY 424 aaaaagaaagcagtcacagtgltgylcccaaaactaacgcccgtgtgcacataaa 483  
DB 14436 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14377  
OY 484 agatcattgaagaaagacaaataaagcgaaataataataatgaatgaactcccttcc 543  
DB 14376 CTCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14317  
OY 544 gaattacttaagaaataacataaagcaaaagaaagagatcaaggtaataaagagc 603  
DB 14316 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14257  
OY 604 attctgtgaagaacacatgagacataagatgataagaaagattgtgctcttata 663  
DB 14256 ATACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14199  
OY 664 ttttttattcaactgaattacat 689  
DB 14198 CATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14173  
RESULT 11  
AAF81465/c  
ID AAF81465 standard; DNA: 631 BP.  
XX  
XX  
XX AAF81465:  
XX  
XX  
XX DT 08-JUN-2001 (first entry)  
XX  
XX DE Corn promoter clone #700333814.  
XX  
XX KM Corn; promoter; transgenic plant; herbicide resistance; ds.  
XX  
XX OS Zea mays.  
XX  
XX PN W0200119976-AZ.  
XX  
XX PD 22-MAR-2001.  
XX  
XX PF 13-SEP-2000; 2000WO-US25078.  
XX  
XX PR 16-SEP-1999; 99US-0154182.  
XX  
XX PA (MONS ) MONSANTO CO.  
XX  
XX PI Anderson HM, Chay CA, Chen G, Conner TW;  
XX  
XX DR WPI: 2001-244796/25.  
XX  
XX PT Novel promoter nucleic acid sequences useful for regulating  
PT heterologous gene expression in plants, comprising regulatory sequences  
PT located upstream to plant DNA structural coding sequences  
XX  
XX  
XX PS Claim 1; Pages 93-94; 101pp; English.  
XX  
XX  
XX The present invention relates to novel corn promoter sequences (see  
CC AAF81465-AAF81478). The promoter sequences are useful for conferring  
CC expression of a second polynucleotide molecule in a transgenic plant  
CC tissue. In addition, the promoter sequences are useful for providing  
CC plants with herbicide resistance. The promoter sequences are suitable for  
CC selectively modulating expression of any operatively linked gene and  
CC provide additional regulatory element diversity in a plant expression  
CC vector in gene stacking approaches. The present sequence is one such corn  
CC promoter sequence isolated in the present invention.  
XX  
XX  
XX Sequence 631 BP; 196 A; 146 C; 120 G; 169 T; 0 other:  
SQ  
Query Match 5.6%; Score 54.2; DB 22; Length 631;  
Best Local Similarity 78.3%; Pred. No. 0.026;

Matches 65; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 890 gtgtcggggaccataatagggtaccctcaaggctcctaattcttcagctggttaacccaa 949  
 Db 130 GTGTCGGGGACCAATTAATGAGGTAACTCAAGACTCCTAATCTACACTGGTAACTTCA 71  
 Oy 950 tcaagcataaagctgcacaaagcct 972  
 Db 70 TCACGACCAAGCTGCACAAAGTCT 48

RESULT 12  
 AAC86507/c  
 ID AAC86507 standard; DNA; 2722 BP.

AAC86507;  
 19-MAR-2001 (first entry)

DE DNA comprising a barley promoter and Agrobacterium ipt gene.

XX temporal gene expression; spatial gene expression; plant seed;  
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;  
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;  
 IPT; ss.

XX Synthetic.  
 OS Hordeum vulgare.  
 OS Agrobacterium tumefaciens.  
 OS Zea mays.

PN WO200063401-A1.

PD 26-OCT-2000.

PF 13-APR-2000; 2000WO-US09943.

PR 16-APR-1999; 99US-0129844.

PA (PION-) PIONEER HI-BRED INT INC.

PI Haben JE, Zinselmeier C, Tomes D;

XX WPI; 2000-672743/65.

PT Novel recombinant DNA construct useful for producing transgenic plants  
 having enhanced levels of cytokinin expression, improved stress  
 tolerance and yield stability -

XX Disclosure; Page 69-70; 76pp; English.

XX The present sequence represents a recombinant DNA molecule of the  
 CC invention. It comprises, in this order, a barley promoter, an  
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize  
 CC terminator. The DNA molecules of the invention comprise a genetic  
 CC construct consisting of a promoter directing temporal and/or spatial  
 CC gene expression in plant seed operatively linked to a cytokinin  
 CC modulating gene. The recombinant DNA molecules are useful for producing  
 CC fertile, transgenic plants capable of regulated expression of a  
 CC cytokinin modulating gene in developing seeds. They are also useful  
 CC for improving stress tolerance and yield stability in plants. The  
 CC preferential expression of recombinant DNA molecules of the invention  
 CC occurs about 14-25 days after pollination. The transgenic plants thus  
 CC produced have enhanced levels of cytokinin expression exhibit improved  
 CC seed size, decreased tip kernel abortion and increased seed set during  
 CC unfavourable environmental conditions.

XX Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 other;

Query Match 5.68; Score 54.2; DB 21; Length 2722;  
 Best local Similarity 65.08; Pred. No. 0.032;  
 Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Oy 152 atatatlltagaccttaattgtatgtctatataccaagaagacataaacttagaca 211  
 Db 2561 ATTGTTTATGTTCTTACATTTTTCGTATATCTAATAATGATGATTAACAAATTTGA 2502

Oy 212 tatataaacaataatgaatgtagatgtatgatactataatgacaaagactaa 271  
 Db 2501 CATATACAGMAAACATATATTCATTTATTTAAACTATTTAAAGGTTTAAACGTTTAA 2442

Oy 272 tat 274  
 Db 2441 TTT 2439

RESULT 13  
 AAC86508/c  
 ID AAC86508 standard; DNA; 2722 BP.

AAC86508;

19-MAR-2001 (first entry)

DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.

XX temporal gene expression; spatial gene expression; plant seed;  
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;  
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;  
 IPT; ss.

XX Synthetic.  
 OS Zea mays.  
 OS Agrobacterium tumefaciens.  
 OS Solanum tuberosum.

PN WO200063401-A1.

PD 26-OCT-2000.

PF 13-APR-2000; 2000WO-US09943.

PR 16-APR-1999; 99US-0129844.

PA (PION-) PIONEER HI-BRED INT INC.

PI Haben JE, Zinselmeier C, Tomes D;

XX WPI; 2000-672743/65.

PT Novel recombinant DNA construct useful for producing transgenic plants  
 having enhanced levels of cytokinin expression, improved stress  
 tolerance and yield stability -

XX Disclosure; Page 70-71; 76pp; English.

XX The present sequence represents a recombinant DNA molecule of the  
 CC invention. It comprises, in this order, a maize promoter, an  
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a Solanum  
 CC tuberosum terminator. The DNA molecules of the invention comprise a  
 CC genetic construct consisting of a promoter directing temporal and/or  
 CC spatial gene expression in plant seed operatively linked to a cytokinin  
 CC modulating gene. The recombinant DNA molecules are useful for producing  
 CC fertile, transgenic plants capable of regulated expression of a  
 CC cytokinin modulating gene in developing seeds. They are also useful  
 CC for improving stress tolerance and yield stability in plants. The  
 CC preferential expression of recombinant DNA molecules of the invention  
 CC occurs about 14-25 days after pollination. The transgenic plants thus  
 CC produced have enhanced levels of cytokinin expression exhibit improved  
 CC seed size, decreased tip kernel abortion and increased seed set during  
 CC unfavourable environmental conditions.

XX Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 other;





CC used to row seeds, especially cereals, that have an endosperm with an  
CC increased content of the preselected amino acid, and therefore having an  
CC increased nutritional value. The transformed cereals can be used in feed  
CC formulations for animals. Transforming plants to have an elevated level  
CC of a preselected amino acid in the endosperm of its seed is advantageous  
CC in production of feed formulations. Feed formulations currently require  
CC supplementation with specific amino acids to provide animals with  
CC essential nutrients, which are necessary for their growth. The methods  
CC increase the nutritional content of seeds without detrimental side  
CC effects such as allelopathy or anti-nutritional quality. The  
CC nutritional content of the seeds is increased whilst maintaining a high  
CC yield. The amount of preselected amino acid in the seed is increased at  
CC least 10-20% by weight to about 10 times greater compared to a  
CC wild-type. The amount of preselected amino acid in the seed is increased at  
CC least 10-20% by weight to about 10 times greater compared to a  
CC corresponding untransformed seed. The present sequence represents a  
CC chimeric gene construct produced in the construction of the HT21 gene,  
CC which is derived from the barley (*Hordeum vulgare*) alpha-hordeothionin  
CC gene and introduces 12 lysine residues into the mature protein.

XX Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 other:

XX Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 other;  
SQ

Query Match

5.68; Score 54.2; DB 20; Length 5173;

Best Local Similarity 65.0%; Pred. No. 0.035;  
Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

152 atatatcttagaccttaattgtgctctattcnaaaagatgcataaatctagaca 211

Db 2773 AATTTGTTTACTCTTAGAATTTTTTTCGCTATATCTAAATGCATGATACAAATTAGA 2714

QY 212 tatataaaacacatacatctaagtatctgtgaatctatcaaaatgctaaacgactaa 271

Db 2713 CATATACAGAAACATATATCAATTATTGTATAAACCTATTAAAAAGGTTAAACGTTAA 2654

Oy 272 cat 274

Db 2653 1 1 2651

Search completed: September 9, 2002, 03:23:34  
Job time: 9501 sec

Job time: 950.1 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 23:09:28 Search time 1695.72 Seconds  
(without alignments)  
7736.560 Million cell updates/sec

Title: US-09-763-329-1  
Sequence: 972  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estbda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	91	9.4	496	9	AM120150 614085E09
C 2	89.8	9.2	593	9	AM146803 614085E09
C 3	89.8	9.2	658	9	AM126456 614072D04
C 4	89	9.2	592	12	A2916532
C 5	86	8.8	509	12	BH224464
C 6	86	8.8	536	12	BH224464
C 7	82.2	8.5	589	9	AM231854
C 8	82.2	8.5	781	10	BG320733
C 9	81.8	8.4	933	12	BH128804
C 10	81.4	8.4	498	10	BF728645
C 11	78.8	8.1	548	12	BH414177
C 12	76.4	7.9	535	10	BM267973
C 13	76.4	7.9	553	10	BM332810
C 14	74	7.6	583	9	A1677352
C 15	72.2	7.4	341	12	BH230702
C 16	72	7.4	483	12	BH126949
C 17	72	7.4	805	10	BG320273

18	70.8	7.3	530	12	BH127544	BH127544 G-1b6.r M
C 19	70.6	7.3	573	10	BM739373	BM739373 MEST304-F
C 20	70.4	7.2	268	12	BH623339	BH623339 1007101E0
C 21	70.4	7.2	621	12	BH221445	BH221445 1006101C0
C 22	69.6	7.2	646	12	BH374273	BH374273 AG-ND-155
C 23	69.4	7.1	365	12	BH18745	BH18745 1006081H0
C 24	69.4	7.1	357	12	BH128442	BH128442 G-3e7.r M
C 25	69.2	7.1	661	12	BH254956	BH254956 LDH10BAM0
C 26	68.8	7.1	1101	12	CNS00EVL	AL069706 Drosoph11
C 27	68.8	7.1	478	12	A0844816	A0844816 an34e03 J
C 28	68.4	7.0	469	12	BH623526	BH623526 1007106F0
C 29	68.4	7.0	679	10	BM340527	BM340527 MEST327-G
C 30	68.2	7.0	306	12	BH225597	BH225597 1006127B0
C 31	68	7.0	612	9	AW000135	AW000135 614058B05
C 32	68	7.0	818	12	BH128809	BH128809 G-3e7 M1
C 33	67.8	7.0	312	12	BH127219	BH127219 G-10118.r
C 34	67.8	7.0	875	12	BH327873	BH327873 G-2e1 M1
C 35	67.8	7.0	963	10	BG837788	BG837788 Zm10.0590
C 36	67.8	7.0	1101	12	CNS00EVL	AL069706 Drosoph11
C 37	67.4	6.9	572	12	BH411224	BH411224 1007022B0
C 38	66.2	6.8	205	12	BH218171	BH218171 1006077F0
C 39	66.2	6.8	463	12	BH127288	BH127288 G-10e21.r
C 40	66.2	6.8	474	12	BH127387	BH127387 G-1b5.r M
C 41	66.2	6.8	529	12	BH621078	BH621078 1007104E0
C 42	65.8	6.8	1101	12	CNS0039C	AL069921 Drosoph11
C 43	65	6.7	560	9	A1739978	A1739978 605075B04
C 44	64.6	6.6	503	12	BH227306	BH227306 1006138H0
C 45	64.4	6.6	585	9	AM126514	AM126514 614101F07

## ALIGNMENTS

RESULT 1  
LOCUS AM120150/c 496 bp mRNA linear EST 22-OCT-1999  
DEFINITION 614085E09.y1 614 - root cDNA library from walbot lab zea mays cDNA,  
mRNA sequence.  
ACCESSION AM120150  
VERSION AM120150.1 GI:6095483  
KEYWORDS EST  
SOURCE Zea mays.  
ORGANISM Zea mays.  
REFERENCE 1 (bases 1 to 496)  
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC  
clade: Panicoideae: Andropogoneae: Zea.  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
UNIVERSITY  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 8227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614085 row: E column: 09.  
Location/Qualifiers  
1..496  
/organism="Zea mays"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
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/tissue\_type="root"  
/dev\_stage="3-4 days old"  
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lab (LM)"  
BASE COUNT 143 a 88 c 83 g 181 t 1 others  
ORIGIN

Query Match	9.4%	Score 91	DB 9	Length 496
Best Local Similarity	63.6%	Pred. NO. 1.1e-05		
Matches 175	Conservative	0	Mismatches 90	Indels 10
			Gaps	2
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Db	301	TTACCAATTACTCCCGACGATCCCAAAATACATTCGTGTTTAGCTCTGATTAAGTCT	242	
QY	181	attatcaaaagaaatgcataataatctagaacataataataaaacatacttaagatgc	240	
Db	241	ATATATCAAAATAGTGATGTGATGAAATTTAGACACATRTATTAAGCAGCATACATCAAGCTTG	182	
QY	241	tatgaatcattcaaaatgcuaaaacgacbaabatatatggagcggagggagttacttatta	300	
Db	181	TATGAATTCCTTATATATCTAAACAAAATTTTAAATTTGGGCGACAGGGAGTATCACACAGAT	122	
QY	301	gtgagatfacatgtaattcttctctatcttcacaataataagcttggtcttca----tcaac	357	
Db	121	GGAGGACATTAATATTAGACTAATTATAGCAAAAGAAAGAAATCTGTATATAAACCTGAAC	62	
QY	358	aactatataattacacatgtccaaacatttgaattat	392	
Db	61	TAAAGTAGATCAATATATAAACCTAAGAAATCAAT	27	

FEATURES	source
LOCUS	AM146803/c
DEFINITION	593 bp MRNA linear EST 03-NOV-1999
ACCESSION	AM146803
VERSION	614085ED09.y2 614 - root cDNA library from Walbot Lab Zea mays cDNA.
KEYWORDS	AM146803
SOURCE	AM146803.1 GI:6194699
ORGANISM	EST. Zea mays. Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 593) Walbot, V. Maize ESTs from various cDNA libraries sequenced at Stanford University Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 614085 row: E column: 09. Location/Qualifiers 1..593

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/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LW)"
BASE COUNT      175 a      105 c      100 g      213 t
ORIGIN
Query Match      9.2%   Score 89.8;   DB: g;   Length 593;
Best Local Similarity 74.6%   Pred. No. 1.6e-05;
Matches 129; Conservative 0; Mismatches 37; Indels 7; Gaps 1;

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Oy 128 ttatcccttgaatccctaaagtcaccaata------tttagaccttaaatgtagtgc 180  
 Db 334 TTACCACTTACTOCCCTCAGTCCCAAAATACATTGCGTTTGAAGCGCTGATGTTCAATGTC 265  
 Oy 181 attatcaaaaagaatgcaataaatactagaacatactataaaaacacatcccttaagtctg 240  
 Db 264 ATATTCAAATATGCTGATGATGAATTTAGACACATATATAAAGCATTACATCAAGTGTG 205  
 Oy 241 taatgatactaataaatgcataaagcaactaatatctagggagggagggatgc 293  
 Db 204 TATTAATCCATTATATATCTTAATAACAAATTTTATATTTGGGCGACAGGAGAGTAC 152

RESULT	3			
LOCUS	AM126456/c			
DEFINITION	AM126456 614072D04.y2 614 - root cDNA library from Walbot Lab Zea mays cDNA.	658 bp	mRNA	linear EST 22-OCT-1995
ACCESSION	AM126456			
VERSION	AM126456			
KEYWORDS	AM126456.1 GI:6101986			
SOURCE	EST			
ORGANISM	Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 658)			
REFERENCE				

TITLE	JOURNAL	COMMENT	FEATURES	SOURCE
Malize ESTs from various cDNA libraries sequenced at Stanford University	Unpublished (1999)	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 614072 row: D column: 04.	location/Qualifiers 1..658 /organism="Zea mays" /cultivar="W23" /db_xref="taxon:4577" /clone_lib="614 - root cDNA library from Walbot Lab" /tissue_type="root" /dev_stage="3-4 days old" /lab_host="XLOLR" /note="organ: root; Vector: p Bluescript II SK+, Site_1: EcoRI, Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)";	190 a 119 c 119 g 230 t

Query Match	9.2%	Score 89.8	DB 9	Length 658
Best Local Similarity	74.6%	Pred. NO. 1,66-05		
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			Gaps	1

  

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QY	181	atattcaaaagaatgacaaataaactctagacatatatacaaacacacatttaagtatc	240
DB	251	attttcaaatagtgatgattgattgatttagacacattttatnaagcattacattcaagtggtg	192
QY	241	tatgaatctttaaataatgcttaaaacagacaaatataatggtgcgaaggaattac	293
DB	191	tatcaattccattatattatctttaaacaatttttaattttgggcccagagggagatc	139

  

RESULT	4
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DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
A2916522	Pc1L7_B10-s-1-fwd_0	Maize PstI B73	leaf	Zea mays genomic, DNA	
A2916522	GI:13347802				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 592)				
TITLE	Missouri Maize Project--Maize Mapping Project.				
JOURNAL	PstI Zea mays B73 PstI leaf tissue library				
COMMENT	Unpublished (2001)				
	Contact: Schroeder S				
	Missouri Maize Project--Maize Mapping Project				
	University of Missouri				
	209 Curtis Hall, Columbia, MO 65211, USA				
	Tel: 573 882 6214				
	Fax: 573 884 7850				
	Email: sschroeder@celep.hals.agron.missouri.edu				
	Class: shotgun.				
FEATURES	Location/Qualifiers				
source	1..592				
	/organism="Zea mays"				
	/cultivar="B73"				
	/db_xref="taxon:4577"				
	/clone_lib="Maize PstI B73 Leaf"				
	/tissue_type="Leaf"				
	/lab_host="DH5 alpha"				
	/note="Organ: Leaf; Vector: pUC19; PstI digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to pUC19 transformed in DH5 alpha"				
BASE COUNT	204 a 103 c 114 g 170 t 1 others				
ORIGIN					
Query Match	9.2%; Score 89; DB 12; Length 592;				
Best Local Similarity	78.1%; Pred. No. 2.2e-05;				
Matches 107; Conservative	0; Mismatches 30; Indels 0; Gaps 0;				
OY	162 gacctaataatgcatctatattcaaaagaatgacataaacttgacatatataaa 221				
DB	275 GTCCGCAAAATATATATCTATATTTAAATGGATATGATGACATCAATATACAA 334				
OY	222 aacatacattaaagatgcatgaatcattataaaatgctaaacagactaatatagga 281				
DB	335 ACCATGCGATCATATATATGATGACACCTACTAATTAACCTAAACGACTACTATTTGGA 394				
OY	282 cggagggaggaactttat 298				
DB	395 CGAAGGAGCTAGTATTT 411				
RESULT	5				
LOCUS	BH224464 509 bp DNA linear GSS 08-NOV-2001				
DEFINITION	1006119C01.x2 1006 - RescueMu Grid G Zea mays genomic, DNA				
ACCESSION	BH224464				
VERSION	BH224464				
KEYWORDS	GSS.				
SOURCE	GSS.				
ORGANISM	Zea mays.				
	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 509)				
AUTHORS	Walbot V.				
TITLE	Maize genomic sequences found using engineered RescueMu transposon				
JOURNAL	Unpublished (2001)				

```

COMMENT
Contact: Malhot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: valhotestanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006119 row: 44
Class: transposon-tagged

FEATURES
SOURCE
    location/Qualifiers
    1..509
        /organism="Zea mays"
        /cultivar="mixed background W23/A188/B73"
        /db_xref="taxon:4577"
        /clone_lib="1006 - Rescuemu Grid G"
        /tissue_type="leaf"
        /dev_stage="adult"
        /lab_host="DH10B"
        /note="Organ: Leaf; Vector: Rescuemu (engineered from
        plasmidscript backbone); Site_1: BamHI; Site_2: BglII;
        Rescuemu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription
        units. For more information on Rescuemu, go to the web
        site 'www.zmdb.iastate.edu' and follow the links for
        'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was
        extracted from leaf punches, double digested using BamHI
        and BglII, and ligated to form circular plasmids. DH10B
        cells were transformed and then screened on LB plates with
        ampicillin."
172 a 70 c 102 g 165 t

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[illegible]

SOURCE ORGANISM	REFERENCE
<i>Zea mays</i> .	1 (pages 1 to 536)
<i>Zea mays</i>	Walbot, V.
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC Clade: Panicoideae: Andropogoneae: Zea.	unpublished (2001)
	Contact: Walbot V
	Department of Biological Sciences

```

FEATURES
SOURCE
    Email: valbot@stanford.edu
    Possible ligation site of ends cut by 2 different endonucleases.
    Reverse complemented post-ligation sequence from source sequence.
    Plate: 1006059   row: 7
    Class: transposon-tagged
    location/Qualifiers
        1..336

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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescuemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: leaf; Vector: Rescuemu (engineered from
pluiscrypt backbone); Site_1: BamHI; Site_2: BglII;
Rescuemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuemu, go to the web
site 'www.emdb.iastate.edu' and follow the links for
'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

Query Match	8.8%	Score 86:	DB 12:	Length 536:
Best Local Similarity	57.1%	Pred. No. 7.1e-05:		
Matches 176:	Conservative	0:	Mismatches 130:	Indels 2:
			Gaps	
OY	1	tttttatactctccctacatccatttttcgaagaaccatctactccctcaagtc	150	
Db	107	TCCTTTCTGCTTAAAAAAATATATAATATGAGTATGTAATATCTCTCTCCCAATAATAG	166	
OY	151	ataatactttagaaccttaaatctgatactatataccaagaagacaataaactagac	210	
Db	167	CAGCATTTTAAAGCTCAGATTTTATATGCTATATATTCATATGATGATTTAGCAAGATTAAC	226	
OY	211	ataataataaacaacatacttaagatctgtatctgatactataataatgctcaaaagacata	270	
Db	227	ATATATNTAGACACTATACATCATATATATATATGATTTAATTAATAAAAGTAAATATGATT	286	
OY	271	acataataggaacggaggagtaactataatagtagatactacatctgtattttctctatcca	330	
Db	287	TTAATTTTGGAGCGAGGAGGAGTACTATTTTCATGTTTTATGGC--TCCAAATTAATTTTATTTATA	344	
OY	331	ataataatctcgtttttccaatccaataataatacttaaccaatgccaacaacatttgaat	390	
Db	345	AAGATATATTTCGTATTTAATCTAATAATATATTTATTAGATCATCAATCGATTTATTTG	404	
OY	391	ataataatcct	398	
Db	405	ATATTTCT	412	

RESULT	7
AM231854/c	
LOCUS	AM231854
DEFINITION	687060B02.x3 687 - Early embryo from Delaware Zea mays cDNA, mRNA
ACCESSION	AM231854
VERSION	AM231854
KEYWORDS	EST.
SOURCE	Zea mays.
ORGANISM	Zea mays.

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
1 (bases 1 to 589) Walbot,V. Maize ESTs from various cDNA libraries sequenced at Stanford University	Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 687060 row: B column: 02.

FEATURES  
 SOURCE  
 Location/Qualifiers  
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 /organism="Zea mays"  
 /cultivar="Illinois High Oil"  
 /db\_xref="taxon:4577"  
 /clone\_lib="687 Early embryo from Delaware"  
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 /dev\_stage="14, 21, 28, and 35 days after pollination"  
 /lab\_host="E. coli SOLR"  
 /note="Organ: embryo; Vector: pBluescript SK; Site: 1: XhoI  
 /; Site: 2: EcoRI; Library was prepared by Stratagene using  
 the Uni-Zap XR system (Stratagene BN937328-12). Clones  
 were picked by a Q-bot after blue/white selection  
 (ampicillin resistance - use 100 micrograms/microliter).  
 Developed from a pool of equal amounts of RNA from  
 developing embryos sampled at 14, 21, 28 and 35 days after  
 pollination of the Illinois High Oil Maize Strain Cycle  
 90. This closed strain has been selected for high oil  
 concentration for 90 generations and originates from the  
 1890s era open pollinated variety Burr's white"  
 149 a 145 c 149 g 146 t

Query Match	8.5%;	Score 82.2;	DB 9;	length 589;
Best Local Similarity	96.6%;	Pred. No. 0.00029;		
Matches	84;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
OY	1	tagaagatatttggtgtgtatcgaataabaagtatgacatgcacgtgtagactcattat	60	
Db	88	TAGAAATATATTTGTTGTTTACCGAATATATAGTTGCATATCCATCGCTGTGACTCATATAT	29	
OY	61	taacacataaacaagaattccctcttatt	87	
Db	28	TAACATAATAAACCGATTTCCTCTTTT	2	
RESULT	8			
LOCUS	781 bp	MRNA	linear	EST 27-FEB-2001
DEFINITION	zmo4.06h05_R zmo4.AAFC ECORC cold stressed_maze-seedlings Zea mays			
ACCESSION	BCG320733			
VERSION	BCG320733.1	GI:13150411		
KEYWORDS	EST.			
SOURCE	Zea mays.			





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/clonetype="MES177-H02"
/tissue="Zea mays"
/clone_lib="ISUM5-RN"
/lab_host="DH10B"
/notes="Vector: pT73PAC; Site 1: EcoRI; Site 2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cytokinin-treated seedlings, callus, Anaerobic treated seedlings,
Brassinolide-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGGAAGAAATTCGCGCCGCGAGAAATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
BASE COUNT      144 a      141 c      130 g      120 t
ORIGIN
Query Match      7.9% Score 76.4; DB 10; Length 535;
Best Local Similarity 84.5%; Pred. No. 0.0026;
Matches 98; Conservative 0; Mismatches 16; Indels 2; Gaps 1;
Qy 153 tatatttagacctaaattgctatctatctaaagaatgacaataatctagacat 212
Db 9 TTTTTCGCGCACTTAATTTTATCTATATCTAATTAATGATTAATTAATCTACAC-- 66
Qy 213 atataaacaacatacattagatctatgataatcattataaataatctaaacgac 268
Db 67 ATATATAAACACATGATTAAGTTTGTATGATCAATTAATGCTAAACACGAC 122

RESULT 13
BM332810      553 bp      mRNA      linear      EST 16-JAN-2002
LOCUS      MES177-H02.T3 ISUM5-RN Zea mays cDNA clone MES177-H02 3', mRNA
DEFINITION      sequence.
ACCESSION      BM332810
VERSION      BM332810.1 GI:18162971
KEYWORDS      EST.
SOURCE      Zea mays.
ORGANISM      Zea mays.
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 553)
Men T.J., Qiu F., Guo L., Ashlock, D.A. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

```

```

Individual basecall and confidence value were assigned using the
phred software.
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/software/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
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/clone="MES177-H02"
/clone_lib="ISUM5-RN"
/tissue="mixture"
/lab_host="DH10B"
/notes="Vector: pT73PAC; Site 1: EcoRI; Site 2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cytokinin-treated seedlings, callus, Anaerobic treated seedlings,
Brassinolide-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGGAAGAAATTCGCGCCGCGAGAAATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
BASE COUNT      148 a      145 c      136 g      124 t
ORIGIN
Query Match      7.9% Score 76.4; DB 10; Length 535;
Best Local Similarity 84.5%; Pred. No. 0.0026;
Matches 98; Conservative 0; Mismatches 16; Indels 2; Gaps 1;
Qy 153 tatatttagacctaaattgctatctatctaaagaatgacaataatctagacat 212
Db 9 TTTTTCGCGCACTTAATTTTATCTAATTAATGATTAATTAATCTACAC-- 66
Qy 213 atataaacaacatacattagatctatgataatcattataaataatctaaacgac 268
Db 67 ATATATAAACACATGATTAAGTTTGTATGATCAATTAATGCTAAACACGAC 122

RESULT 14
A1677352
LOCUS      A1677352 583 bp      mRNA      linear      EST 02-FEB-2000
DEFINITION      605053H02.x1 605 - Endosperm cDNA library from Schmidtd lab Zea mays
cDNA, mRNA sequence.
ACCESSION      A1677352

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VERSION A1677352.1 GI:4886232  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC  
 clade: Panicoideae: Andropogoneae: Zea.  
 1 (bases 1 to 583)  
 Walbot, V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 Unpublished (1999)  
 JOURNAL Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 60503 row: H column: 02.  
 FEATURES  
 source location/Qualifiers  
 1..583  
 /organism="Zea mays"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="605 - Endosperm cDNA library from Schmidt lab"  
 /tissue\_type="nucellar, embryo, and endosperm"  
 /dev\_stage="10-14 days post-pollination"  
 /lab\_host="DH5(alpha)"  
 /note="Organ: Kernel; Vector: PAD-GAL4-2'; Site.1: EcoRI;  
 Site.2: XhoI; Kernel endosperm cDNA library from Schmidt  
 lab"  
 BASE COUNT 148 a 130 c 156 g 149 t  
 ORIGIN  
 Query Match 7.6%; Score 74; DB 9; Length 583;  
 Best Local Similarity 100.0%; Pred. No. 0.0063;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 tagaataattgtgtatcgaaataagttgacagccatcgctgtgtaaccattat 60  
 |||||||  
 Db 74 TAGAAATATTGTCTGTATCGAATATGATTGATGCCATCCGCTGATCAATTAT 15  
 |||||||  
 Oy 61 taacataaascaa 74  
 |||||||  
 Db 14 TAACATATAAACCA 1  
 |||||||  
 RESULT 15  
 BH230702 341 bp DNA linear GSS 08-NOV-2001  
 LOCUS 1006159B04.x1 1006 - Rescuemu Grid G Zea mays genomic, DNA  
 DEFINITION sequence.  
 ACCESION BH230702  
 VERSION BH230702.1 GI:16834165  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC  
 clade: Panicoideae: Andropogoneae: Zea.  
 1 (bases 1 to 341)  
 Walbot, V.  
 Maize genomic sequences found using engineered Rescuemu transposon  
 Unpublished (2001)  
 JOURNAL Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation  
 sequence submitted separately.  
 Plate: 1006159 row: 18  
 Class: transposon-tagged.  
 FEATURES  
 source location/Qualifiers  
 1..341  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1006 - Rescuemu Grid G"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: Rescuemu (engineered from  
 paluescript backbone); Site.1: BamHI; Site.2: BglII;  
 Rescuemu is a 4.9 kb, modified maize mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on Rescuemu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."  
 BASE COUNT 97 a 79 c 80 g 85 t  
 ORIGIN  
 Query Match 7.4%; Score 72.2; DB 12; Length 341;  
 Best Local Similarity 78.7%; Pred. No. 0.015;  
 Matches 111; Conservative 0; Mismatches 28; Indels 2; Gaps 2;  
 Oy 834 gtgcgacgtacaaattgtataaattatatttattcccaattctatg-cattgtg 892  
 |||||||  
 Db 103 GAGCAACTTAATATGTTTACAAATACTCTTAATTAATTAATTAATTAACCTG 162  
 |||||||  
 Oy 893 tcgggagcaataataggggtaccccaaggctcccaattctcagctgtgaa-ccccalc 951  
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 Db 163 TCGCGACGCAATATATGAGGGGTACCCCAAGGCTCTAATTCGTAGCTGAACCCCAAC 222  
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 Oy 952 agcataagctgcacaagcct 972  
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 Db 223 AGCATTAAGCTGCATAAGGCT 243  
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Search completed: September 9, 2002, 02:45:00  
 Job time: 12932 sec



10/10/2002 10:10:10 AM

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 00:31:03 : Search time 49.9 seconds  
(without alignments)  
4784.685 Million cell updates/sec

Title: US-09-763-329-1  
Sequence score: 972  
1 tagaataattgtgtgtat.....gcataaagctgcaagcct 972

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/prodata/2/lna/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/lna/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/lna/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/lna/CTOS.COMB.seq:\*  
6: /cgn2\_6/prodata/2/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.8	7.0	2661	1 US-08-351-413-1	Sequence 1, Appl
2	67.8	7.0	2661	2 US-09-025-583-1	Sequence 1, Appl
3	44.4	4.6	658	4 US-08-998-416-595	Sequence 595, Appl
4	42.6	4.4	4427	4 US-08-796-101-12	Sequence 12, Appl
5	42.2	4.3	7218	1 US-08-232-463-14	Sequence 14, Appl
6	41.6	4.3	19124	2 US-08-487-826B-13	Sequence 13, Appl
7	41.2	4.2	19124	2 US-08-487-826B-13	Sequence 13, Appl
8	41.2	4.2	2049	2 US-08-417-210A-116	Sequence 116, Appl
9	41.2	4.2	2989	2 US-08-566-398-9	Sequence 9, Appl
10	41.2	4.2	3208	2 US-08-566-398-9	Sequence 9, Appl
11	41.2	4.2	3209	1 US-08-105-483-220	Sequence 220, Appl
12	41.2	4.2	3209	1 US-08-220-151-62	Sequence 62, Appl
13	41.2	4.2	3209	1 US-08-413-118-62	Sequence 62, Appl
14	41.2	4.2	3209	1 US-08-224-391-90	Sequence 90, Appl
15	41.2	4.2	3209	1 US-08-484-304-90	Sequence 90, Appl
16	41.2	4.2	3209	1 US-08-224-657-39	Sequence 39, Appl
17	41.2	4.2	3209	1 US-08-709-209-220	Sequence 220, Appl
18	41.2	4.2	3209	1 US-08-458-101-220	Sequence 220, Appl
19	41.2	4.2	3209	2 US-08-184-009-68	Sequence 68, Appl
20	41.2	4.2	3209	2 US-08-486-968-27	Sequence 27, Appl
21	41.2	4.2	3209	2 US-08-417-210A-66	Sequence 66, Appl
22	41.2	4.2	3209	2 US-08-458-356-66	Sequence 66, Appl
23	41.2	4.2	3209	2 US-08-471-025-27	Sequence 27, Appl
24	41.2	4.2	3209	3 US-08-658-665-27	Sequence 27, Appl
25	41.2	4.2	3209	3 US-08-473-446-62	Sequence 62, Appl
26	41.2	4.2	3209	4 US-08-796-101-43	Sequence 43, Appl
27	41.2	4.2	3209	4 US-08-460-736-68	Sequence 68, Appl

C 28	41	4.2	3209	4 US-09-085-273-27	Sequence 27, Appl
C 29	41	4.2	3209	4 US-09-354-138-39	Sequence 39, Appl
C 30	41	4.2	3209	5 PCT-US96-00547-27	Sequence 27, Appl
C 31	41	4.2	3460	2 US-08-658-665-57	Sequence 57, Appl
C 32	41	4.2	3460	4 US-08-796-101-21	Sequence 21, Appl
C 33	41	4.2	3460	4 US-09-085-273-57	Sequence 57, Appl
C 34	41	4.2	3652	2 US-08-658-665-60	Sequence 60, Appl
C 35	41	4.2	3652	4 US-08-796-101-24	Sequence 24, Appl
C 36	41	4.2	3622	4 US-09-085-273-60	Sequence 60, Appl
C 37	41	4.2	3750	3 US-08-617-860B-19	Sequence 19, Appl
C 38	41	4.2	4427	2 US-08-658-665-48	Sequence 48, Appl
C 39	41	4.2	4427	4 US-09-085-273-48	Sequence 48, Appl
C 40	40.6	4.2	872	4 US-08-998-416-487	Sequence 487, Appl
C 41	40.2	4.1	2096	1 US-08-458-084-1	Sequence 1, Appl
C 42	40.2	4.1	2096	1 US-08-205-508-1	Sequence 1, Appl
C 43	40.2	4.1	2096	1 US-08-278-630A-10	Sequence 10, Appl
C 44	40.2	4.1	2096	5 PCT-US95-02945-1	Sequence 1, Appl
C 45	40.2	4.1	2116	1 US-07-811-048-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-08-351-413-1  
Sequence 1, Application US/08351413  
Patent No. 5750867  
GENERAL INFORMATION:  
APPLICANT: Williams, Mark  
APPLICANT: Leemans, Jan  
TITLE OF INVENTION: Maintenance of male-sterile plants  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: 810 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 2046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,413  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/899,072  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/970,849  
FILING DATE: 03-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-102PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2661 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays

STRAIN: Inbred line W-22  
PUBLICATION INFORMATION:  
AUTHORS: Hamilton et al.,  
JOURNAL: Sex Plant Reprod.  
VOLUME: 2  
PAGES: 208-  
DATE: 1989  
US-08-351-413-1

Query Match 7.0%; Score 67.8; DB 1; Length 2661;  
Best Local Similarity 96.4%; Pred. No. 1.7e-07;  
Matches 80; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 891 tctcggggaccataattagggtaccctcaagctcccaattctcagctgtacc-ca 949  
Db 2325 tctcggggaccataattagggtaccctcaagctcccaattctcagctgtacc-ca 2384  
OY 950 tcagcataaagctgcgaagcct 972  
Db 2385 TCAGCGTAAAGCTGCAAGGCCT 2407

## RESULT 2

US-09-025-583-1  
Sequence 1, Application US/09025583  
Patent No. 5977433  
GENERAL INFORMATION:  
APPLICANT: Williams, Mark  
TITLE OF INVENTION: Maintenance of male-sterile plants  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 2046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,583  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,413  
FILING DATE:  
APPLICATION NUMBER: US 07/899,072  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/970,849  
FILING DATE: 03-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-102PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2661 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
ORGANISM: Zea mays  
STRAIN: Inbred line W-22  
PUBLICATION INFORMATION:  
AUTHORS: Hamilton et al.,  
JOURNAL: Sex Plant Reprod.  
VOLUME: 2  
PAGES: 208-  
DATE: 1989  
US-09-025-583-1

Query Match 7.0%; Score 67.8; DB 2; Length 2661;  
Best Local Similarity 96.4%; Pred. No. 1.7e-07;  
Matches 80; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 891 tctcggggaccataattagggtaccctcaagctcccaattctcagctgtacc-ca 949  
Db 2325 tctcggggaccataattagggtaccctcaagctcccaattctcagctgtacc-ca 2384  
OY 950 tcagcataaagctgcgaagcct 972  
Db 2385 TCAGCGTAAAGCTGCAAGGCCT 2407

## RESULT 3

US-08-998-416-595  
Sequence 595, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippson, Peter  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 595:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 658 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)



```

1 NAME: BENT, Stephen A.
2 REGISTRATION NUMBER: 29,768
3 REFERENCE/DOCKET NUMBER: 30472/114 IMM
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (703)836-9300
6 TELEFAX: (703)683-4109
7
8 TELE: 899149
9
10 INFORMATION FOR SEQ ID NO: 14:
11
12 SEQUENCE CHARACTERISTICS:
13     LENGTH: 7218 base pairs
14     TYPE: nucleic acid
15     STRANDEDNESS: single
16     TOPOLOGY: linear
17
18 IMMEDIATE SOURCE:
19     CLONE: pTZspt-F15
20
21 US-08-232-463-14

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Query Match      4.38; Score 42.2; DB 1; Length 7218;
Best Local Similarity 7.68; Pred. No. 0.26;
Matches 23; Conservative 156; Mismatches 124; Indels 0; Gaps 1.
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Oy	345	tcttcaacatcacaataatattaccacatcccaacatttgaaattatatcatcgctgc	404
Db	1479	TTACCAATCTGTGCAAGTAGTTAAAGATAGAACAATTGGTCACRRRRRRRRRRRRR	14200
Oy	405	agcacccgtgcacgaatcgtaaaagaagcagtcaggctgctgccaaaaactaatgcgc	464
Db	1419	RR	13600
Oy	465	cgttcgtgcacctataaagctctcggagaagaccaaaataagycatatattaatg	524
Db	1359	RR	13000
Oy	525	taatatgacctcccctcttgaattcctcggataaacccaagcaaaaaaaaaagagaa	584
Db	1299	RR	12400
Oy	585	gatcaaggtaaatlaaagagcctctcggaaaacacctgagacataaagtcatlaagta	644
Db	1239	RR	11800
Oy	645	tga gaa	
Db	1179	RRA RRA	1177

RESULT 6  
 US-08-487-826B-13  
 : Sequence 13, Application US/08487826B  
 : Patent No. 5993827  
 : GENERAL INFORMATION:  
 : APPLICANT: Sim, Kim L.  
 : APPLICANT: Chltnis, Chetan  
 : APPLICANT: Miller, Louis H.  
 : APPLICANT: Peterson, David S.  
 : APPLICANT: Su, Xin-zhan  
 : APPLICANT: Wellens, Thomas E.  
 : TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
 : TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
 : NUMBER OF SEQUENCES: 45  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Knobbé Martens Olson & Bear  
 : STREET: 620 Newport Center Drive 16th floor  
 : CITY: Newport Beach  
 : STATE: California  
 : COUNTRY: US  
 : ZIP: 92660  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentln Release #1.0 version #1.25

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/487,826B
3 FILING DATE: 10-SEP-1993
4 CLASSIFICATION: 435
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Israel, Ned
7 REGISTRATION NUMBER: 29,655
8 REFERENCE/DOCKET NUMBER: NH121.001CPI
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (619) 235-8550
11 TELEFAX: (619) 235-0176
12 INFORMATION FOR SEQ. ID NO.: 13:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 19124 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA
19 HYPOTHETICAL: NO
20 ANTI-SENSE: NO
21
22 US-08-487-826B-13

```

Query Match	4.38;	Score 41.6;	DB 2;	Length 19124;
Best Local Similarity	48.18;	Pred. No. 0.45;		
Matches 149;	Conservative 0;	Mismatches 159;	Indels 2;	Gaps 1;

[illegible]

RESULT 7  
 US-08-487-826B-13/c  
 : Sequence 13, Application US/08487826B  
 : Patent No. 5993827  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Sim, Kim L.  
 : APPLICANT: Chitnis, Chetan  
 : APPLICANT: Miller, Louis H.  
 : APPLICANT: Peterson, David S.  
 : APPLICANT: Su, Xin-zhaun  
 : APPLICANT: Wellens, Thomas E.  
 :  
 : TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VITAX  
 : TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERITHROCYTE BINDING PROTEINS  
 :  
 : NUMBER OF SEQUENCES: 45  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Knobb Martens Olson & Bear  
 : STREET: 620 Newport Center Drive 16th Floor  
 : CITY: Newport Beach  
 : STATE: California  
 : COUNTRY: US  
 :  
 : ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CPI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-487-826B-13

Query Match 4.28; Score 41.2; DB 2; Length 19124;  
Best Local Similarity 48.68; Pred. No. 0.56;  
Matches 201; Conservative 0; Mismatches 208; Indels 5; Gaps 3;

OY 26 aalgaatgacatgcgcgctgactcatatlaaacaagaattccctta 85  
DB 4625 AATTACTATATAGTATTTATATATGATATTTCCATTTTAAAGTTTGTG 4566  
OY 86 ttatcttllatctc-ccctacatcttggcaagccatctccttacccta 144  
DB 4565 TCATCAATATTTATATATATATATATATATATATATATATATATATAT 4506  
OY 145 agtccaatatattlaaaccttaattglatgcatatlaacaagaatgcacaat 204  
DB 4505 AATCTTAAATCTTTTAAATATATATATATATATATATATATATATATAT 4446  
OY 205 ctagaacatataataaacacatcatgaattgtaigaatcclataaalgctaaa 264  
DB 4445 TTAGACACAAATATATATATATATATATATATATATATATATATATAT 4386  
OY 265 cgactaatattatggacgaggaaglaacttattagtagtaacttacttctct 324  
DB 4385 TAATATAAATAATTTATGTGACA-TTATGCTTAATTTTATATATATTTTAT 4327  
OY 325 attccaataataagtcugatttcaatcatatataatataatccagtcacaacat 384  
DB 4326 ATTCTTATATATATATTTTATATATATATATATATATATATATATATAT 4267  
OY 385 tgaattatatactagtgacagcctcgacgacgacgacgacgacgacgacgac 438  
DB 4266 ---ATTATATATATCTTACCAACATTTATATATATATATATATATATAT 4216

RESULT 8  
US-08-417-210A-116/c  
Sequence 116, Application US/08417210A  
Patent No. 5863542  
GENERAL INFORMATION:  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: TARAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
TITLE OF INVENTION: IMMUNOEFFICIENCY RECOMBINANT FOXYVIRUS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.

STREET: 530 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,210A  
FILING DATE: 05-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2690  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-840-3333  
INFORMATION FOR SEQ ID NO: 116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2049 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-417-210A-116

Query Match 4.28; Score 41; DB 2; Length 2049;  
Best Local Similarity 45.98; Pred. No. 0.36;  
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

OY 85 attatcttllatctctccatccatcttggcaagccatctccttacccta 144  
DB 397 AATGACATTTATGCTATGTCGTAACCAATATATATATATATATATATATAT 338  
OY 145 agtccaatatatttgaaccttaatttgaatgctatataatcaagaatgaataat 204  
DB 337 TCTTATATCTTGGCATTTCTGTAATGTAATGTAAGAGTATACATATACGAT 278  
OY 205 ctagaacatataataaacacacatcatgaattgtagtaacttacttctctct 264  
DB 277 ATATACAGGTAT 218  
OY 265 cgactaatattatggacgaggaaglaacttattagtagtaacttacttctct 324  
DB 217 TTCCTTATATATTTTATATGTTTATGTTATTTGTTAGGTTATACAAAATATAT 158  
OY 325 attccaataataagtcugatttcaatcaatcaatataatataatccagtcacaacat 384  
DB 157 TGTGTATTTTAAAGCCTCGTTAAGATTAAGCTTATATATATATATATATAT 98  
OY 385 tgaat 389  
DB 97 GTAGT 93

RESULT 9  
US-08-566-398-9/c  
Sequence 9, Application US/08566398  
Patent No. 5858373  
GENERAL INFORMATION:  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: GETTIG, RUSSELL  
TITLE OF INVENTION: RECOMBINANT FOXYVIRUS - FELINE INFECTIOUS  
PERTONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR  
MAKING AND USING THEM  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
STREET: 530 Fifth Avenue





```

STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO.: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-220

```

```

Query Match      4.2% Score 41: DB 1: Length 3209;
Best Local Similarity 45.9%: Pred. No. 0.4:
Matches 140: Conservative 0: Mismatches 165: Indels 0: Gaps 0:

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OY 85 attatcctttatatactccctacatcatttggcaagccattaccctaccctc 144
DB 384 AATAGCATTTATGCTATGCTGACCAATATGATGACAGATTCCTTAATACGTA 325
OY 145 agtcccaataattttagacctaaatgtatgtctatataccaagaatgacaat 204
DB 324 TCTTATTATCTCTGCAATATGCTAATGTAATGTAAGATATGATACGATATAG 265
OY 205 ctgaagacataataaacaacatataagtaagtatgaatcattaaatgctaaa 264
DB 264 ATATACGCTGATATTAATTTAAACCCATTCTGAGTAATAATTAATGATATTACAT 205
OY 265 cgactaatatattggaagcgaggaacttattagtagatcacattgtatttctc 324
DB 204 TTCCTTTATTTATTTATGTTTATGTTATGTTAGTTATGCAAAAATTAATGTTATT 145
OY 325 attccaaataaagtcgttcttcaatcaacaalataatataccatcccaacatt 384
DB 144 TGTGTATATTAAAGCGCTGAAGATAAGCTTAGTTAACATATATGCTTAGCTTTT 85
OY 385 tgaat 389
DB 84 GTAGT 80

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RESULT 12
US-08-220-151-62/c
Sequence 62, Application US/08220151
Patent No. 5529780
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
NUMBER OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESS: CURTIS, MORRIS & SAFFORD
STREET: 530 Fifth Avenue

```

```

CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
JTELEX: 425066 CURTMS
INFORMATION FOR SEQ. ID NO.: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-220-151-62

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```

Query Match      4.2% Score 41: DB 1: Length 3209;
Best Local Similarity 45.9%: Pred. No. 0.4:
Matches 140: Conservative 0: Mismatches 165: Indels 0: Gaps 0:

```

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OY 85 attatcctttatatactccctacatcatttggcaagccattaccctaccctc 144
DB 384 AATAGCATTTATGCTATGCTGACCAATATGATGACAGATTCCTTAATACGTA 325
OY 145 agtcccaataattttagacctaaatgtatgtctatataccaagaatgacaat 204
DB 324 TCTTATTATCTCTGCAATATGCTAATGTAATGTAAGATATGATACGATATAG 265
OY 205 ctgaagacataataaacaacatataagtaagtatgaatcattaaatgctaaa 264
DB 264 ATATACGCTGATATTAATTTAAACCCATTCTGAGTAATAATTAATGATATTACAT 205
OY 265 cgactaatatattggaagcgaggaacttattagtagatcacattgtatttctc 324
DB 204 TTCCTTTATTTATTTATGTTTATGTTATGTTAGTTATGCAAAAATTAATGTTATT 145
OY 325 attccaaataaagtcgttcttcaatcaacaalataatataccatcccaacatt 384
DB 144 TGTGTATATTAAAGCGCTGAAGATAAGCTTAGTTAACATATATGCTTAGCTTTT 85
OY 385 tgaat 389
DB 84 GTAGT 80

```

```

RESULT 13
US-08-413-118-62/c
Sequence 62, Application US/08413118
Patent No. 5688920
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
NUMBER OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: CURTIS, MORRIS & SAFFORD, P. C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR

```

Page 8

ADDRESS: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/224,391  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/729,800  
FILING DATE: 17-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3209 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-224-391-90

Query Match	4.28;	Score 41;	DB 1;	Length 3209;
Best Local Similarity	45.98;	Pred. No. 0.4;		
Matches 140;	Conservative	0;	Mismatches 165;	Indels 0;
			Gaps	0.

Qy	85	atlaaccttllatatctcctccatccatttttgaaagcccatlacccttacccca	14
Db	384	AATACCAATTTTCACATATGCTGCTACCCCAATTCATGACAGAAATTCCTTAATACGTAA	32
Qy	145	agluccaatataattttagacccttaaatgtatgctatataccaagaatgacaataat	20
Db	324	TCTATTTATCTCTTGCAATTCGTAAATAGTAATTTGAAGAGTAATACCAATTAAGATTAAG	26
Qy	205	ctcagacataatataaacacatataatgaatgatgtatgaaacatataaagctcaaa	26
Db	264	ATTTCACGATATTTAAATATTTAAACCCCATCTCGATGATTAATATTACGATATTACAT	20
Qy	265	cgacataacttaaggagcgagggagtaacttatttgatgatgcattgtatattctct	32
Db	204	TTCTCTTTATTTATTTTATCTTTAGTATTATTTGTTAGTTATACAAAATATATCTTATT	14
Qy	325	atcccaatatagaatcctgattttccaacaaatcatatataatcattgccaacatct	38
Db	144	TCTGTATATTTAAAGCGCTGTTAAGAAATACCTTAAATACATATTATATCGCTAGCTTTT	85
Qy	385	tgaaat 389	
Db	84	GTAAGT 80	

US-08-484-304-90/C  
Sequence 90. Application US/08484304  
Patent No. 5744141  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Pincus, Steven E.  
TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,304  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/224,391  
FILING DATE:  
APPLICATION NUMBER: US/07/729,800  
FILING DATE: 17-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
TELECOMMUNICATION INFORMATION:  
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INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3209 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-484-304-90

Query Match 4.2%; Score 41; DB 1; Length 3209;  
Best Local Similarity 45.9%; Pred. No. 0.4;  
Matches 140; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 85 attaccctttatctccctccatccatttgcgaagccattatcccttaccctta 144  
DB 384 AATAGCATTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTA 325  
QY 145 agtcccaatataatttgacccttaattgtagtctatattcaagaagatgaataat 204  
DB 324 TCTTATTAATCTTCTGCAATTCCTAATGTAATGTAAGATTAACGATTAACG 265  
QY 205 ctgaacatatataaacaacacacataagatattgtagtctatctataaalgctaa 264  
DB 264 ATATACAGTATATTAATTAATTAACCCCATTCCTGAGTAATAATAATTAACAT 205  
QY 265 cgaactaatatattggaagaggaagtagtactattagtagattacattgtattctct 324  
DB 204 TTCCCTTTATTTATTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 145  
QY 325 attccaataataagtcggttttcaatacaataatattacatattccatgccaataatlt 384  
DB 144 TGTGTAATTTAAAGCTCGTTAAGATTAAGCTTACTTAACATATTATCGCTTACGTTT 85  
QY 385 tgaat 389  
DB 84 GTAGT 80

Search completed: September 9, 2002, 02:46:17  
Job time: 8114 sec

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